AMENDMENTS TO THE SPECIFICATION:

Please replace original paragraph [0023] with the following amended paragraph.

[0023] Figure 7. A: The alignment of the gram-positive promoter consensus with the sequence determined from "PCR walk 6-9" of the GP1223 insert.
B. A sequence (SEQ ID NOS: 48-49) containing dyad symmetry followed by a stretch of thymidine residues, approximately 150 nucleotides upstream of the -35 region, that conforms to a prokaryotic factor-independent RNA polymerase terminator sequence.

Please replace paragraph [0037] with the following amended paragraph.

[0037] TABLE 1. Bacterial strains, plasmids and oligonucleotides

Strain, plasmid or oligo	Relevant markers and characteristics	SEQ ID NO.	Reference or source
Strains			
E. coli			
INVαF	F *end*A1 *rec*A1 *hsd*R17(r_k^-, m_k^+) *sup*E44 *thi*-1 *gyr*A96 *rel*A1Ö80*lac*ZÄM15 Ä(*lac*ZYA-*arg*F)U169		Invitrogen
XL1 Blue	*rec*A1 *end*A1 *gyr*A96 *thi*-1 *hsd*R17 *sup*E44 *rel*A1 *lac* [F *pro*AB *lac*I^{q}ZÄM15 Tn10 (Tet^r)] [c]		Stratagene
S. gordonii			
V288	Wild Type (ATCC 35105)		ATCC
GP1223	M protein recombinant strain that expresses M6 protein (*S. pyogenes*) residues 1 to 16 fused to residues 222-441 and contains an *aphIII* gene, Km^r		G. Pozzi
SP-02	M protein recombinant strain, p635:M/*aph*III in V288, Km^r		This work
SP-04	M protein recombinant strain, pLacG:M/*aph*III in V288, Km^r		This work
635/ermC	M protein recombinant strain, p635/ermC in V288, Em^r		This work
LacG/ermC	M protein recombinant strain, pLacG/ermC in V288, Em^r		This work
Plasmids			
pCR2.1	Km^r, Amp^r		Invitrogen
pCR2.1:635	1.1-kb PCR-amplified 6-35 walk from V288 cloned into pCR2.1 at EcoRI, Amp^r		This work
p635(NdeI)	NdeI site incorporated in between orf 1 and orf 2 in pCR2.1:635, Amp^r		This work

Strain, plasmid or oligo	Relevant markers and characteristics	SEQ ID NO.	Reference or source
pCR2.1:6-86	1733 bp PCR amplified 6-86 walk containing most of the *lacG* gene and part of the *lacE* gene from V288 cloned into pCR2.1 at EcoRI, Amp^r		This work
pLacG	Derivative of pCR2.1 carrying 1.7-kb *lac*E/G cassette with NdeI incorporated within the *lac*G ORF, Amp^r		This work
p635(NdeI) derivatives			This work
p635/ermC	1.2-kb *erm*C fragment from pSMB104 cloned into NdeI site, Amp^r		This work
p635:M/aphIII	2.7-kb M/*aph*III fragment from GP1223 cloned into NdeI site, Amp^r		This work
pLacG derivatives			
pLacG/ermC	1.2-kb *erm*C fragment from pSMB104 cloned into NdeI site, Amp^r		This work
pLacG:M/aphIII	2.7-kb M/*aph*III fragment from GP1223 cloned into NdeI site, Amp^r		This work
Oligonucleotides			
CF4	5' -AATAGGGCTCGAGCGGC- 3'	1	23
CF5	5' -GGATCCTAATACGACTCACTATAGGGC- 3'	2	23
CF6	5' -AATAGGGCTCGAGCGGC- 3'	1	23
CF7	5' -ACCTGCCC-(c3-lcaa-CPG spacer)	3	3
CF35	5' -CGATTCGACATAGAAATAAATTGGAG- 3'	4	3
CF43	5' -GTTTGGTGACCTATAGTCAGTG- 3'	5	3
CF45	5' -TGGATGGCATGAATGTATAGAT- 3'	6	3
TB59	5'-AAAGAAGCATAACATATGTCAAAACAAG-3'	7	This work
TB85	5' -ACACTTCATCACTTTGATACCCCAGA- 3	8	This work
TB86	5'-CCATTTGACCATGAGAAGACATCCATC-3'	9	This work
TB95	5'-AAATCTCCATTTGAATGAAGTGCCTCTGGGG-3'	10	This work
TB96	5'-GTCCACAAAGTGCTCAATATTATCCCGATTGAG-3'	11	This work
TB100	5'-AGGGCGTCAGAGAATCTCCAACCCATATACC- 3'	12	This work
TB103	5'-GGAATTCCATATGCGGATAATAAATATATATAAACG-3'	13	This work
TB104	5'GGAATTCCATATGCGATTCACAAAAAATAGGCACACG 3'	14	This work
TB107	5'-GCAGGAGTGGACGAAGAAGCTCC-3'	15	This work
TB117	5'-GGATCCCATATGTAAGGAGCATAAAAATGGC-3'		This work

Please replace paragraph [0054] with the following amended paragraph

[0054] **TABLE 2. Bacterial strains, plasmids, and oligonucleotides**

Strain, plasmid, or oligonucleotide	Relevant markers and characteristics	Reference or source
Strains		
E. coli		
INVαF'	F' *end*A1 *rec*A1 *hsd*R17(r_k^-, m_k^+) *sup*E44 *thi*-1 *gyr*A96 *rel*A1ö80*lac*ZÄM15 Ä(*lac*ZYA-*arg*F)U169	Invitrogen
S. gordonii Challis		
V288	Wild-type (ATCC 35105)	ATCC
GP204	Spontaneous Sm^r mutant of V288	Pozzi et al., 1988
GP230	Recombinant strain contains the *emm*6 gene (*S. pyogenes*) and an *erm*C gene, Em^r, parent strain (V288)	Pozzi et al., 1992
GP251	Recombinant recipient strain contains the cat gene flanked by 145 bp of *emm*6 gene and 202 bp of *erm*C gene, Cm^r, parent strain (GP230)	Oggioni et al., 1996
GP1214	Recombinant strain that expresses M6 protein (*S. pyogenes*) residues 1 to 16 fused to residues 222-441 and contains an *erm*C gene, Em^r, parent strain (GP251)	Oggioni et al, 1994
GP1218	Recombinant strain that expresses M6 protein (*S. pyogenes*) residues 1 to 16 fused to residues 222-441 and contains an *aph*III gene, Km^r, parent strain (GP1214)	Oggioni et al, 1994
GP1223	Recombinant strain that expresses M6 protein (*S. pyogenes*) residues 1 to 16 fused to residues 222-441 and contains an *aph*III gene, Km^r, and has been converted to Sm^r, parent strain (GP1218)	Oggioni et al, 1994

Strain, plasmid, or oligonucleotide	Relevant markers and characteristics	Reference or source
Plasmids		
pCR2.1	Km^r, Amp^r	Invitrogen
pSMB104	Contains the sequences encoding the CRR of M6 protein (*S. pyogenes*) residues 1 to 16 fused to residues 222-441 in tandem with an MspI/ClaI fragment of pE194 () encoding ermC cloned into pBluescript SK-.	Oggioni et al, 1994
Oligonucleotides		
CF4 (SEQ ID NO: 16)	5'-CTAATACGACTCACTATAGGGCTCGAGCG GCCGCCC GGGCAGGT-3'; Adaptor	Siebert et al, 1995
CF5 (SEQ ID NO: 2)	5'-GGATCCTAATACGACTCACTATAGGGC-3'; AP1	Siebert et al, 1995
CF6 (SEQ ID NO: 1)	5'-AATAGGGCTCGAGCGGC-3'; AP2, SEQ	Siebert et al, 1995
CF7	5'-ACCTGCCC-(C3-Icaa-CPG spacer); AP1	This study
CF8 (SEQ ID NO: 17)	5'-TCTAGAGGTACCTTCTCGTGCTTTGTCCGG -3';PCR (GP1223)	This study
CF9 (SEQ ID NO: 18)	5'-TACCGTCCCCCTAGGAAACACTCTTGCAC-3'; SEQ,PCR (GP1223)	This study
CF10 (SEQ ID NO: 19)	5'-TGACTTACTGGGGATCAAGCCTGATTGGG AG-3';PCR (GP1223)	This study
CF11 (SEQ ID NO: 20)	5'-AAGTACATCCGCAACTGTCCATACTCTGAT G-3'; PCR (GP1223)	This study
CF14 (SEQ ID NO: 21)	5'-GTTTTTCGTGTGCCTATTTTTTGTG-3', SEQ 1223	This study

Strain, plasmid, or oligonucleotide	Relevant markers and characteristics	Reference or source
CF15 (SEQ ID NO: 22)	5'-GAGCGCATCGAAAATGCTGTTG-3'; SEQ, PCR (GP204	This study
CF16 (SEQ ID NO: 23)	5'-CTCAGTGTAAAGAGGAAATCC-3'; SEQ	This study
CF17 (SEQ ID NO: 24)	5'-GAGTTTCAATGGTCTTGTCTGG-3'; SEQ, PCR (GP204, GP1223)	This study
CF18 (SEQ ID NO: 25)	5'-CTTGAAAAGCCTGAGGGCTGGTTAC-3'; SEQ, PCR (GP204)	This study
CF19 (SEQ ID NO: 26)	5'-CTTGACCTTTGGTACCTTTGAC-3'; SEQ	This study
CF20 (SEQ ID NO: 27)	5'-GATAGTCACACGGCTACTCACG-3'; SEQ	This study
CF21 (SEQ ID NO: 28)	5'-CGTGAGTAGCCGTGTGACTATC-3'; SEQ	This study
CF22 (SEQ ID NO: 29)	5'-GTCCATAGAGTTTGGATCCAAG-3'; SEQ	This study
CF23 (SEQ ID NO: 30)	5'-GTCAAAGGTACCAAAGGTCAAG-3'; SEQ	This study
CF24 (SEQ ID NO: 31)	5'-CCAGAAATTCGCGATATGAAC-3'; SEQ	This study
CF25 (SEQ ID NO: 32)	5'-GAATGAATCCAGATAAGGTGC-3'; SEQ	This study
CF26 (SEQ ID NO: 33)	5'-GATATCTTCAACTCATGGGATTAC-3'; SEQ, PCR (GP204)	This study
CF27 (SEQ ID NO: 34)	5'-CAAGATTCTCACCAGTTTTATG-3'; SEQ	This study
CF28 (SEQ ID NO: 35)	5'-GCTGCGATGCTTATGATTACC-3'; SEQ	This study
CF29 (SEQ ID NO: 36)	5'-GCTACCAATGCTGACAATAG-3'; SEQ	This study

Strain, plasmid, or oligonucleotide	Relevant markers and characteristics	Reference or source
CF31 (SEQ ID NO: 37)	5'-CCTAAGCAGTTTCTCAAGTTG-3'; SEQ	This study
CF32 (SEQ ID NO: 38)	5'-CATGTTGCCTATCGTCCAGC-3'; SEQ PCR (GP204, GP1223)	This study
CF35 (SEQ ID NO: 3)	5'-CGATTCGACATAGAAATAAATTGGAG-3'; SEQ, PCR (GP204)	This study
CF36 (SEQ ID NO: 39)	5'-CTATAGTCAGTGTGGTTTAGACAAGC-3'; SEQ	This study
CF39 (SEQ ID NO: 40)	5'-GATTATGCTGAATCAAATAGTC-3', SEQ	This study
CF40 (SEQ ID NO: 41)	5'-GAGCACGATAGTAGTCAATCAC-3'; SEQ	This study
CF41 (SEQ ID NO: 42)	5'-CAATTTTTGACTGATACGATGGC-3'; SEQ	This study
CF42 (SEQ ID NO: 43)	5'-CTGTTCTTCCAACTTTTTCAGC-3'; SEQ	This study
CF43 (SEQ ID NO: 4)	5'-GTTTGGTGACCTATAGTCAGTG-3'; SEQ	This study
CF44 (SEQ ID NO: 44)	5'-ATCTATACATTCATGCCATCCA-3'; SEQ	This study
CF45 (SEQ ID NO: 5)	5'-TGGATGGCATGAATGTATAGAT-3'; SEQ	This study

Please replace paragraph [0062] with the following amended paragraph.

[0062] **The region upstream of the GP1223 insert contains regulatory signals.** Immediately upstream of the GP1223 insert, sequences which conform to the consensus for promoters from gram-positive organisms (DeVos, W.M. 1987 FEMS Microbiol. Rev. 46:281-295; Graves, M.C., and J.C. Rabinowitz. 1986. J. Biol. Chem. 261:11409-11415) were found. The alignment of the gram-positive promoter

consensus with the sequence determined from "PCR walk 6-9" is shown in Figure 7A. This sequence shows the following features in common with the gram-positive promoter consensus: (i) the canonical -35 and -10 sequences; (ii) a spacing between those hexanucleotides of 16 to 18 nucleotides; (iii) the conserved dinucleotide sequence TG, immediately preceding the -10 sequence; and (iv) the AT-rich regions upstream of the -35 sequence (AT-box). Approximately 150 nucleotides upstream of the -35 region, a sequence containing dyad symmetry followed by a stretch of thymidine residues conforms to a prokaryotic factor-independent RNA polymerase terminator sequence (Figure 7B). Also, a region containing five direct repeats, 4 perfect and 1 imperfect, of 18 nucleotides (AGTTTAAAATCTTTATTC)(SEQ ID NO: 4) was observed between the terminator and the promoter sequences (Figure 7B). Upstream of the terminator sequence, the nucleotide sequence of the 881-bp "PCR walk 6-9" also contained a partial ORF (designated ORF2 , see Figure 6) encoding 169 residues with no apparent functional homologies in the databases at present. The sequence of ORF 2 had not terminated when the walk fragment ended at an EcoRV site to which the walking adaptor was ligated.